

Query= SEQ ID NO:43
(1650 letters)

Sequences producing significant alignments:

	Score	E
	(bits)	Value
AC018552.5.95189.106311	<u>569</u>	e-159
AC018552.5.17437.94328	<u>297</u>	1e-77

>AC018552.5.95189.106311
Length = 11123

Score = 569 bits (287), Expect = e-159
Identities = 287/287 (100%)
Strand = Plus / Plus

Query: 1257 atgctggccgtgaaggacaaccatgtacgcctctatcaccgtccacggctactt 1316
|||||||
Sbjct: 5423 atgctggccgtgaaggacaaccatgtacgcctctatcaccgtccacggctactt 5482

Query: 1317 cctcatcacccctttggcatgggtcctggccctgggtctggaaagatcttcac 1376
|||||||
Sbjct: 5483 cctcatcacccctttggcatgggtcctggccctgggtctggaaagatcttcac 5542

Query: 1377 cctgtcccgtgctacagcggtcaaggagcgaaaaagaaccgaaagaagggtgtcaccc 1436
|||||||
Sbjct: 5543 cctgtcccgtgctacagcggtcaaggagcgaaaaagaaccgaaagaagggtgtcaccc 5602

Query: 1437 gctggcccttcgagcctgggtgtgacatgggggtggccatctcacccgttggg 1496
|||||||
Sbjct: 5603 gctggcccttcgagcctgggtgtgacatgggggtggccatctcacccgttggg 5662

Query: 1497 cctctccaccgtctacatcttgcaactttcaactccttgcagg 1543
|||||||
Sbjct: 5663 cctctccaccgtctacatcttgcaactttcaactccttgcagg 5709

Score = 563 bits (284), Expect = e-157
Identities = 284/284 (100%)
Strand = Plus / Plus

Query: 880 aggcttccccggagagggtcaagtcaagaagatccccaaagatccacgtggccctgggt 939
|||||||
Sbjct: 3710 aggcttccccggagagggtcaagtcaagaagatccccaaagatccacgtggccctgggt 3769

Query: 940 ggcagcctgttccctgaatctggccttggtaatgtggggagtggtcaaagg 999
|||||||
Sbjct: 3770 ggcagcctgttccctgaatctggccttggtaatgtggggagtggtcaaagg 3829

Query: 1000 tctgatgctgcctgctggccggggctgtcttccactacttcctgcgtgccttc 1059
|||
Sbjct: 3830 tctgatgctgcctgctggccggggctgtcttccactacttcctgcgtgccttc 3889

Query: 1060 acctggatggccttgaagcctccacctctacctgctcgctgtcagggtttcaacacc 1119
|||
Sbjct: 3890 acctggatggccttgaagcctccacctctacctgctcgctgtcagggtttcaacacc 3949

Query: 1120 tacttcgggactacttcctgaagctgagcctgggtggctgggg 1163
|||
Sbjct: 3950 tacttcgggactacttcctgaagctgagcctgggtggctgggg 3993

Score = 228 bits (115), Expect = 9e-57
Identities = 115/115 (100%)
Strand = Plus / Plus

Query: 768 gagaccacccatggaccagtccacggtgcatatcctcacacgcatctcccaggcgggctg 827
|||
Sbjct: 284 gagaccacccatggaccagtccacggtgcatatcctcacacgcatctcccaggcgggctg 343

Query: 828 tggggtctccatgatcttcctggccttcaccattattcttatgccttcgtagg 882
|||
Sbjct: 344 tggggtctccatgatcttcctggccttcaccattattcttatgccttcgtagg 398

Score = 204 bits (103), Expect = 1e-49
Identities = 103/103 (100%)
Strand = Plus / Plus

Query: 1539 aggtgtttcatctgctgtggttcaccatcttacctccaaagtcaagacaccacagt 1598
|||
Sbjct: 8131 aggtgtttcatctgctgtggttcaccatcttacctccaaagtcaagacaccacagt 8190

Query: 1599 ctcctcctactgcaagattggaccaggcccactccgcatct 1641
|||
Sbjct: 8191 ctcctcctactgcaagattggaccaggcccactccgcatct 8233

Score = 204 bits (103), Expect = 1e-49
Identities = 103/103 (100%)
Strand = Plus / Plus

Query: 666 agggaccactggagactggtcttgagggtctgctccacggaggtcagacctgagggac 725
|||
Sbjct: 43 agggaccactggagactggtcttgagggtctgctccacggaggtcagacctgagggac 102

Query: 726 cgtgtgctgctgtgaccacctgacctttcgccctgctcctg 768
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 103 cgtgtgctgctgtgaccacctgacctttcgccctgctcctg 145

Score = 188 bits (95), Expect = 8e-45
Identities = 95/95 (100%)
Strand = Plus / Plus

Query: 1162 ggcctgcccgcctgatggtcatcggaactggagtgccaacagctacggcctctacacc 1221
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 4169 ggcctgcccgcctgatggtcatcggaactggagtgccaacagctacggcctctacacc 4228

Query: 1222 atccgtgataggagaaccgcacctctggagct 1256
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 4229 atccgtgataggagaaccgcacctctggagct 4263

>AC018552.5.17437.94328
Length = 76892

Score = 297 bits (150), Expect = 1e-77
Identities = 150/150 (100%)
Strand = Plus / Plus

Query: 57 aggtcaggaaaagcccaccgaaggccaagaaacacacctgcctggggagcaacaatgta 116
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 68998 aggtcaggaaaagcccaccgaaggccaagaaacacacctgcctggggagcaacaatgta 69057

Query: 117 cgacatcttcaacttgaatgacaaggcttgcaccaagtgcaggcagtcggcag 176
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 69058 cgacatcttcaacttgaatgacaaggcttgcaccaagtgcaggcagtcggcag 69117

Query: 177 cgactcctgcaatgtggaaaacttgcagag 206
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 69118 cgactcctgcaatgtggaaaacttgcagag 69147

Score = 297 bits (150), Expect = 1e-77
Identities = 150/150 (100%)
Strand = Plus / Plus

Query: 344 aggtccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttccca 403
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 73847 aggtccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttccca 73906

Query: 404 agagcctttcgatccctgccaggcaacaggctgtggccgttggccgtcaccattc 463
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 73907 agagcctttcgatccctgccaggcaacaggctgtggccgttggccgtcaccattc 73966

Query: 464 tggacattggtcaggactctttcaagg 493
||| ||| ||| ||| ||| |||
Sbjct: 73967 tggacattggtcaggactctttcaagg 73996

Score = 283 bits (143), Expect = 2e-73
Identities = 143/143 (100%)
Strand = Plus / Plus

Query: 205 agatactggctaaactacgaggcccacatctgtatgaaggaagggttgacgcagaaggtaac 264
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 71877 agatactggctaaactacgaggcccacatctgtatgaaggaagggttgacgcagaaggtaac 71936

Query: 265 acgccttcctgaaggcttggccagaacactcagcaccaacactgcagaagacttat 324
||| ||| ||| ||| ||| ||| |||
Sbjct: 71937 acgccttcctgaaggcttggccagaacactcagcaccaacactgcagaagacttat 71996

Query: 325 ttctctctggagcccttcaggt 347
||| ||| ||| ||| |||
Sbjct: 71997 ttctctctggagcccttcaggt 72019

Score = 272 bits (137), Expect = 7e-70
Identities = 141/142 (99%), Gaps = 1/142 (0%)
Strand = Plus / Plus

Query: 487 ttca-agggccccggctggcctggagatggcagcggcgtgttgaacaatgcctgg 545
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 74849 ttcacagggccccggctggcctggagatggcagcggcgtgttgaacaatgcctgg 74908

Query: 546 gggtttgagtgtggacaaatgcatgtcaccaagctggctgagcctctggagatcgttt 605
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 74909 gggtttgagtgtggacaaatgcatgtcaccaagctggctgagcctctggagatcgttt 74968

Query: 606 ctctcaccagcgaccgccccct 627
||| ||| ||| ||| |||
Sbjct: 74969 ctctcaccagcgaccgccccct 74990

Score = 119 bits (60), Expect = 6e-24
Identities = 60/60 (100%)
Strand = Plus / Plus

```
Query: 1      atggcgacgcccaggggcctggggccctgtcctgtcctgtccggacctcagg 60
          ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 64026 atggcgacgcccaggggcctggggccctgtcctgtcctgtccggacctcagg 64085
```

Score = 81.8 bits (41), Expect = 1e-12
Identities = 41/41 (100%)
Strand = Plus / Plus

```
Query: 628 aacatgaccctcactgttattctggatgtgactaaagg 668
          ||||||| | | | | | | | | | | | | | | | | | | | |
Sbjct: 75495 aacatgaccctcactgttattctggatgtgactaaagg 75535
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NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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1: AC018552. Homo sapiens chro...[gi:27476108]

Links

LOCUS AC018552 152156 bp DNA linear PRI 03-JAN-2003
 DEFINITION Homo sapiens chromosome 16 clone RP11-405F3, complete sequence.
 ACCESSION AC018552
 VERSION AC018552.6 GI:27476108
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 152156)
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 152156)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (14-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 152156)
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
 TITLE Direct Submission
 JOURNAL Submitted (03-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT On Jan 3, 2003 this sequence version replaced gi:13786352.
 Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
www-shgc.stanford.edu
 Quality: Phrap Quality >=40 99.8% of Sequence;
 Estimated Total Number of Errors is 0.2.
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 /chromosome="16"
 /clone="RP11-405F3"
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 61 caccttctcc ctggcattcc gtggccgagc ctgggttcct ctccgtggag gcactgctcg
 121 ctccccctgg cctacctgg a gggctctgtc tgcccccctgg ccctcaactcc tcccaggaa
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